

## RAW SEQUENCE LISTING.

PATENT APPLICATION: US/09/826,791

DATE: 04/20/2001

TIME: 11:49:11

Input Set : A:\Pc10914a.app  
Output Set: N:\CRF3\04202001\I826791.raw

3 <110> APPLICANT: Pfizer Inc  
 5 <120> TITLE OF INVENTION: Novel Polypeptide  
 7 <130> FILE REFERENCE: PC10914ADAM  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/826,791  
 C--> 10 <141> CURRENT FILING DATE: 2001-04-05  
 12 <150> PRIOR APPLICATION NUMBER: 0008504.3  
 13 <151> PRIOR FILING DATE: 2000-04-05  
 15 <150> PRIOR APPLICATION NUMBER: 60/198,367  
 16 <151> PRIOR FILING DATE: 2000-04-19  
 18 <160> NUMBER OF SEQ ID NOS: 6  
 20 <170> SOFTWARE: PatentIn Ver. 2.0  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 993  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <400> SEQUENCE: 1  
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 30 aagagagaat tttcccaat tttatctg ataataatttt tctggggagt cttggggaaat 120  
 32 ggggtgtcca tatatgtttt cctgcagcct tataagaagt ccacatctgt gaacgttttc 180  
 34 atgctaaatc tggccatttc agatctctg ttataaagca cgcttccctt cagggctgac 240  
 36 tattatctta gaggctccaa ttggatattt ggagacctgg cctgcaggat tatgtcttat 300  
 38 tcctgtatg tcaacatgtt cagcagtatt tatttcctga ccgtgctgag tttgtgcgt 360  
 40 ttcctggcaa tggttcaccc ctttcggctt ctgcattgtca ccagcatcag gagtgcctgg 420  
 42 atcctctgtg ggatcatatg gatccttatac atggcttcctt caataatgtt cctggacagt 480  
 44 ggctctgagc agaacggcag tgcacatca tgcttagagc tgaatctta taaaattgtt 540  
 46 aagctgcaga ccatgaacta tattgcctt gttgtggct gcctgctgcc attttcaca 600  
 48 ctcagcatct gttatctgtt gatcatcgg gttctgttaa aagtggaggt cccagaatcg 660  
 50 gggctgcggg tttctcacag gaaggcactg accaccatca tcatcacctt gatcatcttc 720  
 52 ttctgtgtt tcctgcctta tcacacactg aggaccgtcc acttgacac atggaaagt 780  
 54 gtttatgca aagacagact gcataaaggt ttgttatac cactggcctt ggcagcagcc 840  
 56 aatgcctgtt tcaatccctt gctctattac ttgtgtgggg agaattttaa ggacagacta 900  
 58 aagtctgcac tcagaaaagg ccatccacag aaggcaaaga caaagtgtt tttccctgtt 960  
 60 agtgtgtgtt tgagaaaggg aacaagagta taa 993  
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 64 <211> LENGTH: 330  
 65 <212> TYPE: PRT  
 66 <213> ORGANISM: Homo sapiens  
 68 <400> SEQUENCE: 2  
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 72 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile  
 73 20 25 30  
 75 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu  
 76 35 40 45  
 78 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu  
 79 50 55 60  
 81 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp

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82 65 70 75 80  
 84 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg  
 85 85 90 95  
 87 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe  
 88 100 105 110  
 90 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe  
 91 115 120 125  
 93 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly  
 94 130 135 140  
 96 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser  
 97 145 150 155 160  
 99 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu  
 100 165 170 175  
 102 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val  
 103 180 185 190  
 105 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile  
 106 195 200 205  
 108 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val  
 109 210 215 220  
 111 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe  
 112 225 230 235 240  
 114 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr  
 115 245 250 255  
 117 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val  
 118 260 265 270  
 120 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu  
 121 275 280 285  
 123 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu  
 124 290 295 300  
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 143 <211> LENGTH: 22  
 144 <212> TYPE: DNA  
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 152 <211> LENGTH: 1041  
 153 <212> TYPE: DNA  
 154 <213> ORGANISM: Homo sapiens

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Input Set : A:\Pcl0914a.app  
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157 <221> NAME/KEY: CDS  
158 <222> LOCATION: (1)..(1041)  
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163 1 5 10 15  
165 atg gaa cca aat ggc acc ttc agc aat aac aac agc agg aac tgc aca 96  
166 Met Glu Pro Asn Gly Thr Phe Ser Asn Asn Asn Ser Arg Asn Cys Thr  
167 20 25 30  
169 att gaa aac ttc aag aga gaa ttt ttc cca att gta tat ctg ata ata 144  
170 Ile Glu Asn Phe Lys Arg Glu Phe Phe Pro Ile Val Tyr Leu Ile Ile  
171 35 40 45  
173 ttt ttc tgg gga gtc ttg gga aat ggg ttg tcc ata tat gtt ttc ctg 192  
174 Phe Phe Trp Gly Val Leu Gly Asn Gly Leu Ser Ile Tyr Val Phe Leu  
175 50 55 60  
177 cag cct tat aag aag tcc aca tct gtg aac gtt ttc atg cta aat ctg 240  
178 Gln Pro Tyr Lys Lys Ser Thr Ser Val Asn Val Phe Met Leu Asn Leu  
179 65 70 75 80  
181 gcc att tca gat ctc ctg ttc ata agc acg ctt ccc ttc agg gct gac 288  
182 Ala Ile Ser Asp Leu Leu Phe Ile Ser Thr Leu Pro Phe Arg Ala Asp  
183 85 90 95  
185 tat tat ctt aga ggc tcc aat tgg ata ttt gga gac ctg gcc tgc agg 336  
186 Tyr Tyr Leu Arg Gly Ser Asn Trp Ile Phe Gly Asp Leu Ala Cys Arg  
187 100 105 110  
189 att atg tct tat tcc ttg tat gtc aac atg tac agc agt att tat ttc 384  
190 Ile Met Ser Tyr Ser Leu Tyr Val Asn Met Tyr Ser Ser Ile Tyr Phe  
191 115 120 125  
193 ctg acc gtg ctg agt gtt gtg cgt ttc ctg gca atg gtt cac ccc ttt 432  
194 Leu Thr Val Leu Ser Val Val Arg Phe Leu Ala Met Val His Pro Phe  
195 130 135 140  
197 cgg ctt ctg cat gtc acc agc atc agg agt gcc tgg atc ctc tgt ggg 480  
198 Arg Leu Leu His Val Thr Ser Ile Arg Ser Ala Trp Ile Leu Cys Gly  
199 145 150 155 160  
201 atc ata tgg atc ctt atc atg gct tcc tca ata atg ctc ctg gac agt 528  
202 Ile Ile Trp Ile Leu Ile Met Ala Ser Ser Ile Met Leu Leu Asp Ser  
203 165 170 175  
205 ggc tct gag cag aac ggc agt gtc aca tca tgc tta gag ctg aat ctc 576  
206 Gly Ser Glu Gln Asn Gly Ser Val Thr Ser Cys Leu Glu Leu Asn Leu  
207 180 185 190  
209 tat aaa att gct aag ctg cag acc atg aac tat att gcc ttg gtg gtg 624  
210 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val  
211 195 200 205  
213 ggc tgc ctg ctg cca ttt ttc aca ctc agc atc tgt tat ctg ctg atc 672  
214 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile  
215 210 215 220  
217 att cgg gtt ctg tta aaa gtg gag gtc cca gaa tcg ggg ctg cgg gtt 720  
218 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val  
219 225 230 235 240

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221	tct	cac	agg	aag	gca	ctg	acc	acc	atc	atc	atc	atc	acc	ttg	atc	atc	ttc	768
222	Ser	His	Arg	Lys	Ala	Leu	Thr	Thr	Ile	Ile	Ile	Ile	Leu	Ile	Ile	Phe		
223									245		250					255		
225	ttc	ttg	tgt	ttc	ctg	ccc	tat	cac	aca	ctg	agg	acc	gtc	cac	ttg	acg	816	
226	Phe	Leu	Cys	Phe	Leu	Pro	Tyr	His	Thr	Leu	Arg	Thr	Val	His	Leu	Thr		
227									260		265				270			
229	aca	tgg	aaa	gtg	ggt	tta	tgc	aaa	gac	aga	ctg	cat	aaa	gct	ttg	gtt	864	
230	Thr	Trp	Lys	Val	Gly	Leu	Cys	Lys	Asp	Arg	Leu	His	Lys	Ala	Leu	Val		
231									275		280				285			
233	atc	aca	ctg	gcc	ttg	gca	gca	aat	gcc	tgc	ttc	aat	cct	ctg	ctc		912	
234	Ile	Thr	Leu	Ala	Leu	Ala	Ala	Ala	Asn	Ala	Cys	Phe	Asn	Pro	Leu	Leu		
235									290		295				300			
237	tat	tac	ttt	gct	ggg	gag	aat	ttt	aag	gac	aga	cta	aag	tct	gca	ctc	960	
238	Tyr	Tyr	Phe	Ala	Gly	Glu	Asn	Phe	Lys	Asp	Arg	Leu	Lys	Ser	Ala	Leu		
239									305		310				315		320	
241	aga	aaa	ggc	cat	cca	cag	aag	gca	aag	aca	aag	tgt	gtt	ttc	cct	gtt	1008	
242	Arg	Lys	Gly	His	Pro	Gln	Lys	Ala	Lys	Thr	Lys	Cys	Val	Phe	Pro	Val		
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266						50				55						60		
268	Gln	Pro	Tyr	Lys	Lys	Ser	Thr	Ser	Val	Asn	Val	Phe	Met	Leu	Asn	Leu		
269						65				70						75		80
271	Ala	Ile	Ser	Asp	Leu	Leu	Phe	Ile	Ser	Thr	Leu	Pro	Phe	Arg	Ala	Asp		
272						85				90						95		
274	Tyr	Tyr	Leu	Arg	Gly	Ser	Asn	Trp	Ile	Phe	Gly	Asp	Leu	Ala	Cys	Arg		
275						100				105						110		
277	Ile	Met	Ser	Tyr	Ser	Leu	Tyr	Val	Asn	Met	Tyr	Ser	Ser	Ile	Tyr	Phe		
278						115				120						125		
280	Leu	Thr	Val	Leu	Ser	Val	Val	Arg	Phe	Leu	Ala	Met	Val	His	Pro	Phe		
281						130				135						140		
283	Arg	Leu	Leu	His	Val	Thr	Ser	Ile	Arg	Ser	Ala	Trp	Ile	Leu	Cys	Gly		
284						145				150						155		160
286	Ile	Ile	Trp	Ile	Leu	Ile	Met	Ala	Ser	Ser	Ile	Met	Leu	Leu	Asp	Ser		
287						165				170						175		
289	Gly	Ser	Glu	Gln	Asn	Gly	Ser	Val	Thr	Ser	Cys	Leu	Glu	Leu	Asn	Leu		

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290 180 185 190  
292 Tyr Lys Ile Ala Lys Leu Gln Thr Met Asn Tyr Ile Ala Leu Val Val  
293 195 200 205  
295 Gly Cys Leu Leu Pro Phe Phe Thr Leu Ser Ile Cys Tyr Leu Leu Ile  
296 210 215 220  
298 Ile Arg Val Leu Leu Lys Val Glu Val Pro Glu Ser Gly Leu Arg Val  
299 225 230 235 240  
301 Ser His Arg Lys Ala Leu Thr Thr Ile Ile Ile Thr Leu Ile Ile Phe  
302 245 250 255  
304 Phe Leu Cys Phe Leu Pro Tyr His Thr Leu Arg Thr Val His Leu Thr  
305 260 265 270  
307 Thr Trp Lys Val Gly Leu Cys Lys Asp Arg Leu His Lys Ala Leu Val  
308 275 280 285  
310 Ile Thr Leu Ala Leu Ala Ala Asn Ala Cys Phe Asn Pro Leu Leu  
311 290 295 300  
313 Tyr Tyr Phe Ala Gly Glu Asn Phe Lys Asp Arg Leu Lys Ser Ala Leu  
314 305 310 315 320  
316 Arg Lys Gly His Pro Gln Lys Ala Lys Thr Lys Cys Val Phe Pro Val  
317 325 330 335  
319 Ser Val Trp Leu Arg Lys Glu Thr Arg Val  
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**VERIFICATION SUMMARY**

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Input Set : A:\Pc10914a.app

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L:9 M:270 C: Current Application Number differs, Replaced Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date